

FIGURE 1

Mouse FGF-23

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      10       20       30       40       50       60
ATGCTAGGGACCTGCCCTAGACTCCTGGTGGCGTGCTCTGCACTGTCTGCAGCTGGC
M L G T C L R L L V G V L C T V C S L G

      70       80       90      100      110      120
ACTGCTAGAGCCTATCCAGACACTCCCCATTGCTTGCTCCAACCTGGGAAAGCCTGACC
T A R A Y P D T S P L L G S N W G S L T

      130      140      150      160      170      180
CACCTGTACACGGCTACAGCCAGGACAGCTATCACCTACAGATCCATAGGGATGGTCAT
H L Y T A T A R T S Y H L Q I H R D G H

      190      200      210      220      230      240
GTAGATGGCACCCCCCATCAGACCATCTACAGTGCCTGATGATTACATCAGAGGACGCC
V D G T P H Q T I Y S A L M I T S E D A

      250      260      270      280      290      300
GGCTCTGTGGTGTATAACAGGGACCATGACTCGAAGGTTCTTGATGGATCTCCACGGC
G S V V I T G A M T R R F L C M D L H G

      310      320      330      340      350      360
AACATTTGGATCGCTTCACTTCAGCCCAGAGAATTGCAAGTTCCGCCAGTGGACGCTG
N I F G S L H F S P E N C K F R Q W T L

      370      380      390      400      410      420
GAGAATGGCTATGACGTCTACTGTGCGAGAACATCACTACCTGGTGAGCCCTGGGCC
E N G Y D V Y L S Q K H H Y L V S L G R

      430      440      450      460      470      480
GCCAAGGGCATTTCCAGCCGGCACCAACCCGCCCTCTCCAGTTCTGGCTCGC
A K R I F Q P G T N P P P F S Q F L A R

      490      500      510      520      530      540
AGGAACGAGGTCCCGCTGCTGCACTTCTACACTGTTGCCACGGGCCACACGCGCAGC
R N E V P L L H F Y T V R P R R H T R S

      550      560      570      580      590      600
GCCGAGGGACCCACCCGAGCGCACCCACTGAACGTCTCAAGCCGGCCCCCGGCCACG
A E D P P E R D P L N V L K P R P R A T

      610      620      630      640      650      660
CTCTGTGCTGTATCTGCTCTCGCGAGCTGCCAGCGAGAGGAAGGTGGCCCGAGCC
P V P V S C S R E L P S A E E G G P A A

      670      680      690      700      710      720
AGCGATCCTCTGGGGGTGCTGCGCAGAGGCCGTGGAGATGCTCGGGGGCGGGGAGGC
S D P L G V L R R G R G D A R G G A G G

      730      740      750      760
GCGGATAGGTGTGCCCTTCCAGGTTCTAG
A D R C R P F P R F V *

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FIGURE 2

FIGURE 3

Human FGF-23

	10	20	30	40	50	60
	atgttggggcccgctcaggctctgggtctgtgccttg	tcagcgtctgc	agcatgac			
M	L	G	A	R	L	R
	L	W	V	C	A	L
	C	S	V	C	S	H
	70	80	90	100	110	120
	gtcctcagaggctatccaa	tgcctccc	actgctcggtcc	agctgggtgg	cctgatc	
V	L	R	A	Y	P	N
	A	S	P	L	L	G
	S	S	S	W	G	G
				I		
	130	140	150	160	170	180
	cacctgtacacagccacagcc	caggaa	acagctaccac	ctgcagatcc	cacaaga	atggccat
H	L	Y	T	A	I	A
	A	R	N	S	Y	H
	L	Q	I	H	K	N
				G	H	
	190	200	210	220	230	240
	gtggatggcg	cacccc	atcagaccat	ctacagtgc	ccctgtat	catcagaggatgct
V	D	G	A	P	H	Q
	T	I	Y	S	A	L
	M	I	R	S	E	D
				A		
	250	260	270	280	290	300
	ggctttgttgt	gttacagg	gtgtatgagc	agoagata	ccctctgc	atggatttcagaggc
G	F	V	V	I	T	G
	M	S	R	R	Y	L
	C	M	D	F	R	G
	310	320	330	340	350	360
	aacatttttggatcacactat	ttcgacccgg	gagaactgc	agggttcca	acaccagac	gctg
N	I	F	G	S	H	Y
	F	D	P	E	N	C
	R	F	Q	H	Q	T
				L		L
	370	380	390	400	410	420
	gaaaacgggtacgacgt	ttaccactctc	cgtatcactt	ccctgg	cagtctgg	ccgg
E	N	G	Y	D	V	Y
	H	S	P	Q	Y	H
	F	L	V	S	L	G
				R	G	R
	430	440	450	460	470	480
	gcgaagagagcc	ttctgtcc	aggcatgaa	cccccccc	ctactccc	atgtccgg
A	K	R	A	F	L	P
	G	M	N	P	P	P
	H	N	T	P	I	P
				R	R	H
				T	R	S
	490	500	510	520	530	540
	aggaaatggatccccctaa	ttca	ttcaac	ccccccat	accacgggg	ggcacacccggagc
R	N	E	I	P	L	I
	H	F	N	T	P	H
				I	R	T
				R	R	S
	550	560	570	580	590	600
	gccggggacgactcg	ggggac	ccccct	gaa	ccccgggg	ccggatgacc
A	E	D	D	S	E	R
	D	P	L	N	Y	L
				K	P	R
				R	A	R
				M	T	
	610	620	630	640	650	660
	ccggccccgg	ccctctgt	tcacagg	agctccc	gagcgc	ccggaggaca
P	A	P	A	S	C	S
	S	Q	E	L	P	S
				A	E	D
				N	D	N
				S	S	P
				P	H	A
	670	680	690	700	710	720
	agtggccat	ttgggtgg	tcaggggcggt	cgagt	goaacacgc	acgtggggaa
S	D	P	L	G	V	R
				G	N	G
				R	T	T
				V	H	A
				N	A	G
				T	G	
	730	740	750	760		
	ccggggggctgc	ccccc	ttcgcc	aaagttc	atctag	
P	E	G	C	R	P	F
				A	K	I
				*		

Mouse FGF-23	MLGTCLRLVGVLCTVCSLGTARAYPDTSPLLGSNAGSLTHLYTATARTSYHLQIHRDGH	66
	***. *** * .**.***... ***.*****.**.***.*****.*****.***	
Human FGF-23	MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGLIHLHYTATARNSYHLQIHKNGH	66
	VDGTPHQTIYSALMITSEDAGSVVITGAMTRRFLCMDLHQNIFGSLHFSPENCKFRQHTL	126
	***.*****.*****.*****.*****.*****.*****.*****.*****.*****.*****	
	VDGAPHQTIYSALMIRSEDAGFVVITGVMSSRRYLCMDFRQNIFGSHYFPENCRFQHQL	126
	ENGDVYLSQKHHYLVSLGRAKRIFQP GTNPPPSQFLARRNEVPLLHFYTVRPRRHTRS	186
	*****.*****.*****.*****.*****.*****.*****.*****.*****.*****	
	ENGDVYHSPQYHFLVSLGRAKRAFLPGMNPPPSQFLSRRNEIPLIHFNTPIPRRHTRS	186
	AEDPPERDPLNVLKPRPRATPVPSCSRELPSAEEGPAASDPLGVLRGRGDARGGAGG	240
	***.*****.*****.*****.*****.*****.*****.*****.*****.*****.*****	
	AEDDSERDPLNVLKPRARMTPAPASCQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG	240
	ADRCRPFPRFV 251	
	.. ***.**.	
	PEGCRPFAKFI 251	

FIGURE 4

Human FGF-23	MIGARLRLWVACSVCSMSVLRAYPNASPLLGSSWGG--LIHLYTATAR--NSYHL	53
	...* . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . *	
Human FGF-19	MRSGCVVWHWILAGLWLAVAGRPLAFSDAGPHVHYGHGDPIRLRHLYTSGPHGLSSCFL	60
	QIHKNQHVGDAPHQTIYSALMIRSEDAGFWITGVMSSRRYLCMDFRGNIFGSHYFDPENC	113
	* . . * * * . * . * * . . . * . * * * * * * * . * . * . . . * . . . *	
	RIRADGVVDCARGQSAHSLEIKAVALRTVAIKGVHSVRYLCMGADGKMQQLQYSEEDC	120
	RFQHQTLENGYDVYHSPQYHFLVSLGRAK-RAFLPGMNPPPSQFLSRRNEIPLIHFNTP	172
	* . . . * * * . * . . . * * * . * . . . * . * * * . . . * . . . *	
	AEEEIRPDGYNVRSEKHLRVPVLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLR	180
	IPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCSQLPSAEDNSPMASDPLGVVRGGRV	232
	GHLESDFSSPLETDSDPFGLVTLGLEAVRSPSFEK	216
	NTHAGGTGPEGCRPFAKFI	251

FIGURE 5

Human FGF-23	MIGARLRLWVCALCS-VCSMSVLRAYPNASPLLG-SSWGGGLIHLYTATARNs-YH	52
	***..* . . . * .. * *** .. . ***..* . *	
Human FGF-21	MDSDETGF <small>E</small> HSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYL <small>T</small> DDAQQT <small>E</small> AH	60
	LQIHKNGHV <small>D</small> GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPE	112
	*.**...*.*...* * * .. * . * * .. * * .. * . * .. * . * . * . *	
	LEIREDGT <small>V</small> GGAAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA	120
	CRFQHQTL <small>E</small> NGYD <small>V</small> YHSPQYHFLVSLGRAKRAFLPGMNPPPSQFLSRRNEIPLIHFNTP	172
	*.** .. * . * . * . * . * . * . * . * . * . * . * . * . * . * . *	
	CSFRELLLEDGYNVYQSEAHG <small>L</small> PLHLP <small>N</small> KSP-HRDPAAPRGPARFLPLPGLPPALP--EP	177
	IPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCQELPSAEDNSPMASDPLGVVRGGRV	232
	* .. . * .. * .. * .. *	
	-PGILAPQPPDVGS <small>S</small> DPLSMVGPSQGRSPSYAS	209
	NTHAGGTGPEGCRFAKFI	251

FIGURE 6

*Figure 7*

Codon usage for yeast (highly expressed) genes

AmAcid	Codon	Number	/1000	Fraction	..
Gly	GGG	33.00	0.86	0.01	
Gly	GGA	70.00	1.82	0.02	
Gly	GGT	2672.00	69.62	0.91	
Gly	GTC	171.00	4.46	0.06	
Glu	GAG	277.00	7.22	0.10	
Glu	GAA	2442.00	63.63	0.90	
Asp	GAT	1100.00	28.66	0.48	
Asp	GAC	1211.00	31.55	0.52	
Val	GTG	117.00	3.05	0.04	
Val	GTA	75.00	1.95	0.03	
Val	GTT	1548.00	40.33	0.56	
Val	GTC	1026.00	26.73	0.37	
Ala	GCG	36.00	0.94	0.01	
Ala	GCA	203.00	5.29	0.06	
Ala	GCT	2221.00	57.87	0.65	
Ala	GCC	969.00	25.25	0.28	
Arg	AGG	20.00	0.52	0.01	
Arg	AGA	1336.00	34.81	0.83	
Ser	AGT	116.00	3.02	0.05	
Ser	AGC	94.00	2.45	0.04	
Lys	AAG	2365.00	61.62	0.78	
Lys	AAA	651.00	16.96	0.22	
Asn	AAT	347.00	9.04	0.22	
Asn	AAC	1259.00	32.80	0.78	
Met	ATG	766.00	19.96	1.00	
Ile	ATA	43.00	1.12	0.02	
Ile	ATT	1223.00	31.87	0.52	
Ile	ATC	1070.00	27.88	0.46	
Thr	ACG	28.00	0.73	0.01	
Thr	ACA	126.00	3.28	0.06	

**Figure 7 (continued)**

Thr	ACT	1129.00	29.42	0.50
Thr	ACC	962.00	25.07	0.43
Trp	TGG	325.00	8.47	1.00
End	TGA	10.00	0.26	0.09
Cys	TGT	254.00	6.62	0.89
Cys	TGC	33.00	0.86	0.11
End	TAG	11.00	0.29	0.10
End	TAA	85.00	2.21	0.80
Tyr	TAT	219.00	5.71	0.19
Tyr	TAC	913.00	23.79	0.81
Leu	TTC	2202.00	57.38	0.69
Leu	TTA	576.00	15.01	0.18
Phe	TTT	432.00	11.26	0.27
Phe	TTC	1145.00	29.83	0.73
Ser	TCG	26.00	0.68	0.01
Ser	TCA	149.00	3.88	0.06
Ser	TCT	1279.00	33.33	0.52
Ser	TCC	818.00	21.31	0.33
Arg	CGG	0.00	0.00	0.00
Arg	CGA	1.00	0.03	0.00
Arg	CGT	249.00	6.49	0.15
Arg	CGC	5.00	0.13	0.00
Gln	CAG	62.00	1.62	0.05
Gln	CAA	1225.00	31.92	0.95
His	CAT	236.00	6.15	0.35
His	CAC	433.00	11.28	0.65
Leu	CTG	52.00	1.35	0.02
Leu	CTA	236.00	6.15	0.07
Leu	CTT	90.00	2.35	0.03
Leu	CTC	14.00	0.36	0.00
Pro	CCG	10.00	0.26	0.01
Pro	CCA	1271.00	33.12	0.80
Pro	CCT	279.00	7.27	0.18
Pro	CCC	33.00	0.86	0.02

## Figure 8

Codon usage for *Drosophila* (highly expressed) genes

AmAcid	Codon	Number	/1000	Fraction	..
Gly	GGG	6 00	0.28	0 00	
Gly	GGA	380 00	18.04	0 22	
Gly	GGT	575 00	27.29	0 34	
Gly	GGC	746 00	35.41	0 44	
Glu	GAG	1217 00	57.77	0 91	
Glu	GAA	115 00	5.46	0 09	
Asp	GAT	503 00	23.88	0 43	
Asp	GAC	654 00	31.04	0 57	
Val	GTG	719 00	34.13	0 45	
Val	GTA	29 00	1.38	0 02	
Val	GTT	226 00	10.73	0 14	
Val	GTC	608 00	28.86	0 38	
Ala	GCG	94 00	4.46	0 05	
Ala	GCA	80 00	3.80	0 04	
Ala	GCT	446 00	21.17	0 24	
Ala	GCC	1277.00	60.61	0 67	
Arg	AGG	48 00	2.28	0 06	
Arg	AGA	12 00	0.57	0 01	
Ser	AGT	16 00	0.76	0 01	
Ser	AGC	267 00	12.67	0 23	
Lys	AAG	1360 00	64.55	0 93	
Lys	AAA	108 00	5.13	0 07	
Asn	AAT	127 00	6.03	0 13	
Asn	AAC	878 00	41.67	0.87	
Met	ATG	387 00	18.37	1.00	
Ile	ATA	4.00	0.19	0.00	
Ile	ATT	390 00	18.51	0.29	
Ile	ATC	969.00	45.99	0.71	
Thr	ACG	114 00	5.41	0.08	
Thr	ACA	34 00	1.61	0.02	

**Figure 8 (continued)**

Thr	ACT	164.00	7.78	0.11
Thr	ACC	1127.00	53.49	0.78
Trp	TGG	243.00	11.53	1.00
End	TGA	1.00	0.05	0.01
Cys	TGT	20.00	0.95	0.08
Cys	TGC	220.00	10.44	0.92
End	TAG	12.00	0.57	0.17
End	TAA	58.00	2.75	0.82
Tyr	TAT	113.00	5.36	0.16
Tyr	TAC	574.00	27.25	0.84
Leu	TTG	210.00	9.97	0.12
Leu	TTA	9.00	0.43	0.01
Phe	TTT	62.00	2.94	0.09
Phe	TTC	635.00	30.14	0.91
Ser	TCG	195.00	9.26	0.17
Ser	TCA	29.00	1.38	0.02
Ser	TCT	103.00	4.89	0.09
Ser	TCC	558.00	26.49	0.48
Arg	CGG	7.00	0.33	0.01
Arg	CGA	25.00	1.19	0.03
Arg	CGT	281.00	13.34	0.34
Arg	CGC	465.00	22.07	0.55
Gln	CAG	703.00	33.37	0.91
Gln	CAA	66.00	3.13	0.09
His	CAT	88.00	4.18	0.22
His	CAC	312.00	14.81	0.78
Leu	CTG	1182.00	56.10	0.69
Leu	CTA	21.00	1.00	0.01
Leu	CTT	55.00	2.61	0.03
Leu	CTC	224.00	10.63	0.13
Pro	CCG	84.00	3.99	0.09
Pro	CCA	135.00	6.41	0.15
Pro	CCT	72.00	3.42	0.08
Pro	CCC	626.00	29.71	0.68

## Figure 9

Codon usage for enteric bacterial (highly expressed) genes 7/19/83

AmAcid	Codon	Number	/1000	Fraction
Gly	GGG	13.00	1.89	0.02
Gly	GGA	3.00	0.44	0.00
Gly	GGU	365.00	52.99	0.59
Gly	GUC	238.00	34.55	0.38
Glu	GAG	108.00	15.68	0.22
Glu	GAA	394.00	57.20	0.78
Asp	GAU	149.00	21.63	0.33
Asp	GAC	298.00	43.26	0.67
Val	GUG	93.00	13.50	0.16
Val	GUU	146.00	21.20	0.26
Val	GUU	289.00	41.96	0.51
Val	GUC	38.00	5.52	0.07
Ala	GCG	161.00	23.37	0.26
Ala	GCA	173.00	25.12	0.28
Ala	GCU	212.00	30.78	0.35
Ala	GCC	62.00	9.00	0.10
Arg	AGG	1.00	0.15	0.00
Arg	AGA	0.00	0.00	0.00
Ser	AGU	9.00	1.31	0.03
Ser	AGC	71.00	10.31	0.20
Lys	AAG	111.00	16.11	0.26
Lys	AAA	320.00	46.46	0.74
Asn	AAU	19.00	2.76	0.06
Asn	AAC	274.00	39.78	0.94
Met	AUG	170.00	24.68	1.00
Ile	AUA	1.00	0.15	0.00
Ile	AUU	70.00	10.16	0.17
Ile	AUC	345.00	50.09	0.83
Thr	ACG	25.00	3.63	0.07
Thr	ACA	14.00	2.03	0.04
Thr	ACU	130.00	18.87	0.35
Thr	ACC	206.00	29.91	0.55

**Figure 9 (continued)**

AmAcid	Codon	Number	/1000	Fraction
Trp	UGG	55.00	7.98	1.00
End	UGA	0.00	0.00	0.00
Cys	UGU	22.00	3.19	0.49
Cys	UGC	23.00	3.34	0.51
End	UAG	0.00	0.00	0.00
End	UAA	0.00	0.00	0.00
Tyr	UAU	51.00	7.40	0.25
Tyr	UAC	157.00	22.79	0.75
Leu	UUG	18.00	2.61	0.03
Leu	UUA	12.00	1.74	0.02
Phe	UUU	51.00	7.40	0.24
Phe	UUC	166.00	24.10	0.76
Ser	UCG	14.00	2.03	0.04
Ser	UCA	7.00	1.02	0.02
Ser	UCU	120.00	17.42	0.34
Ser	UCC	131.00	19.02	0.37
Arg	CGG	1.00	0.15	0.00
Arg	CGA	2.00	0.29	0.01
Arg	CGU	290.00	42.10	0.74
Arg	CGC	96.00	13.94	0.25
Gln	CAG	233.00	33.83	0.86
Gln	CAA	37.00	5.37	0.14
His	CAU	18.00	2.61	0.17
His	CAC	85.00	12.34	0.83
Leu	CUG	480.00	69.69	0.83
Leu	CUA	2.00	0.29	0.00
Leu	CUU	25.00	3.63	0.04
Leu	CUC	38.00	5.52	0.07
Pro	CCG	190.00	27.58	0.77
Pro	CCA	36.00	5.23	0.15
Pro	CCU	19.00	2.76	0.08
Pro	CCC	1.00	0.15	0.00

## *Figure 10*

Chromosomal localization of genes of the FGF family in human

Gene	Localization	Gene	Localization
FGF-1	5q31.3-q33.2	FGF-12	3q29-qter
FGF-2	4q26	FGF-13	X
FGF-3	11q13	FGF-14	13
FGF-4	11q13.3	(FGF-15)	
FGF-5	4q21	FGF-16	-
FGF-6	12p13	FGF-17	8p21
FGF-7	15q13-q22	FGF-18	5
FGF-8	10q25-q26	FGF-19	11q13.1
FGF-9	13q11-q12	FGF-20	8p21.3-p22
FGF-10	5p12-p13	FGF-21	19q13.1-qter
FGF-11	17	FGF-22	19p13.3
		FGF-23 □	12p13

Human FGF-15 gene has not been identified. The localization of human FGF-16 gene has not been determined.

*Figure II*

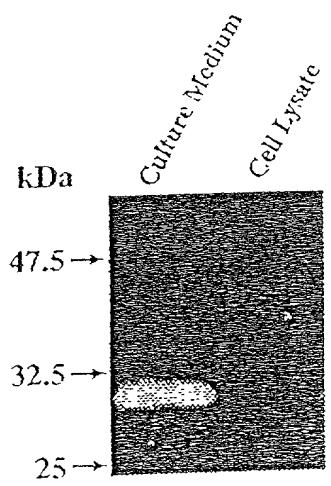
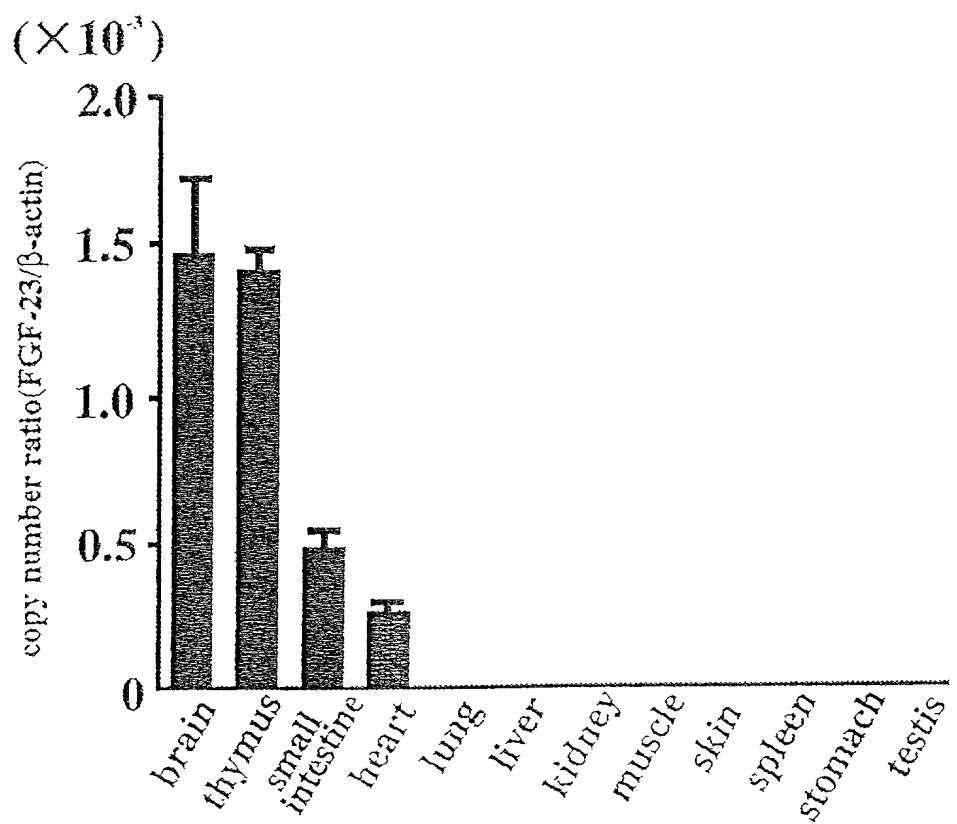


Figure 12



*Figure 13*

Y D C D E D G E T D G H

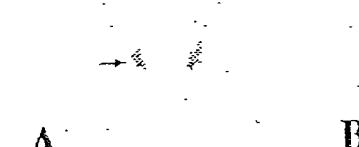
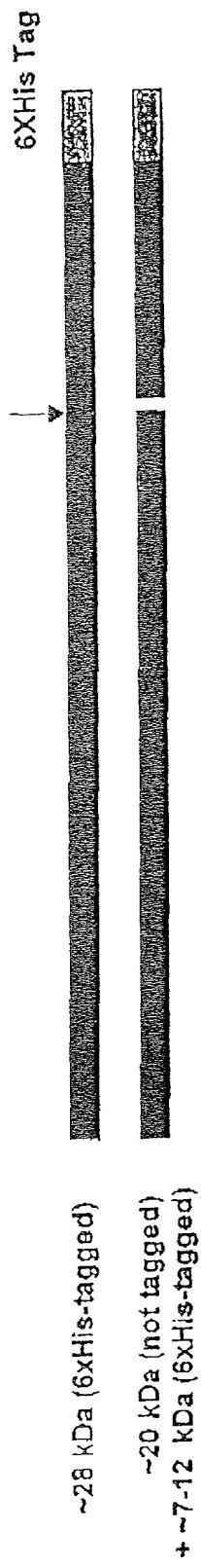


FIGURE 14



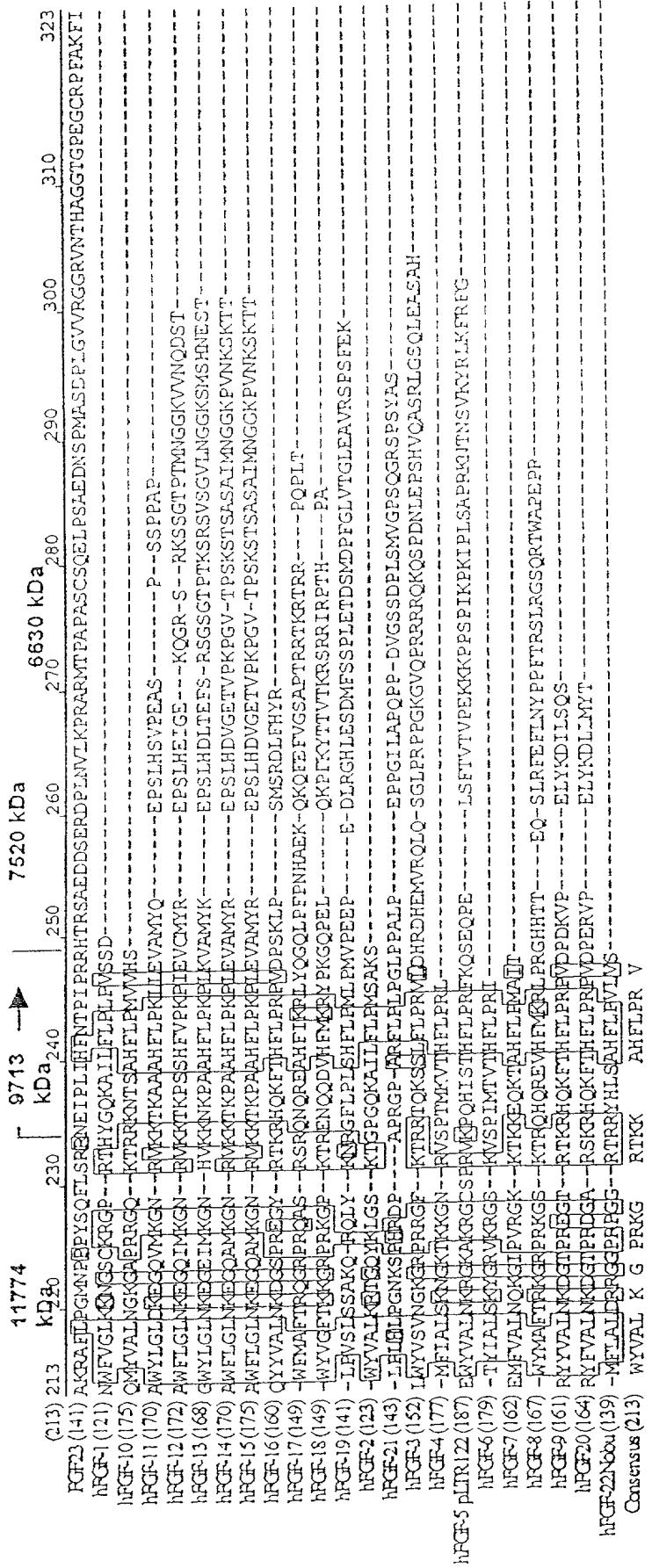


Fig. 15

Figure 16

